

SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

<130> U 015759-8

<140> 10/533,781

<141> 2005-05-04

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 1010

<212> DNA

<213> Pontellina plumata

<400> 1

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<210> 2

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<212> PRT

<213> Pontellina plumata

<400> 2

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 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
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<212> DNA

<213> Pontellina plumata

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tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcacca atgggagaca      480
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<210> 4

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<212> PRT

<213> Pontellina plumata

<400> 4

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          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175

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Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe

180

185

190

Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile

195

200

205

Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala

210

215

220

<210> 5

<211> 814

<212> DNA

<213> Labidocera aestiva

<400> 5

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gagggaaaca aggttatcgg agacttcaag gttggttgat caggattccc agctaacagt    420
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<210> 6

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<212> PRT

<213> Labidocera aestiva

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1

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10

15

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20

25

30

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser

35

40

45

Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
 50 55 60
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe
 165 170 175
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 7

<211> 753

<212> DNA

<213> cf. *Pontella meadi* Wheeler

<400> 7

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 ctccctacct cctctccac attcttggct acggatatta ccactttgca acctccctg 240
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 acaagatcat tggagacttc aagggttggtg gaacaggatt ccctaccaac agtcttatct 420
 tcaactgacaa gatcattaaa tccaacccta cctgtgagaa catgttcccc aaggctgaca 480
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720
753

$\langle 210 \rangle$	8
$\langle 211 \rangle$	222
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	cf.
$\langle 400 \rangle$	8

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			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Ile	Lys	Gly	Pro	Ile	Ser	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
	50					55					60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
65				70					75					80	
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
			85					90					95		
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Ile	Ile	Gly
		100						105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Thr	Asn	Ser	Leu	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
	130					135					140				
Lys	Ala	Asp	Asn	Thr	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
145				150						155				160	
Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Phe
		165						170					175		
Lys	Ser	Ala	Ile	His	Thr	Thr	Met	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
		180					185						190		
Thr	Tyr	Arg	Val	Val	Glu	Glu	Thr	His	Thr	Gln	Asn	Glu	Val	Ala	Ile
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	210					215					220				

<210>	9
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<212>	DNA

<213> cf. *Pontella meadi* Wheeler

<400> 9

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tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt      180
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agtccatcaa aggacctctc tccttctctc cctacctact ctcccacatt cttggctatg      300
gatattacca ctttgcaacc ttccctgctg gatatgaaaa tatctacctt catgccatga      360
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tgcttaaaga tgggtggatac tactctgccc aggttaacaa ccatatgcac ttcaagagtg      660
ccatccatcc tacaatgctc cagaatggtg gatccatggt cactcacaga gtagtagagg      720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta      780
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<210> 10

<211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 10

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Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
          50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
          85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
          100          105          110
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
          115          120          125

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Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
 130 135 140
 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
 145 150 155 160

 Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile
 195 200 205
 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 11
 <211> 847
 <212> DNA
 <213> *Pontella mediterranea*
 <400> 11

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 aaaaaaa 847

<210> 12
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 <212> PRT
 <213> *Pontella mediterranea*
 <400> 12

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			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Tyr	Ala
	50					55					60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Val	Tyr	Leu	His	Ala	Met	Lys	Asn
65					70					75					80
Gly	Gly	Tyr	Ser	Asn	Thr	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
				85					90					95	
Ile	Ser	Ala	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Arg	Gln	Ile	His	Gly
			100					105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Ala	Asp	Ser	Ile	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	His	Ile	Tyr	Pro
	130					135						140			
Lys	Ala	Asn	Asn	Ile	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Trp	Met	Leu
145					150					155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Leu
				165					170					175	
Gln	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Lys	Asn	Gly	Gly	Ser	Met	Phe
			180					185					190		
Thr	Tyr	Arg	Lys	Val	Glu	Glu	Leu	His	Thr	Gln	Thr	Glu	Val	Gly	Ile
		195					200					205			
Val	Glu	Tyr	Gln	His	Val	Phe	Lys	Arg	Pro	Thr	Ala	Phe	Ala		
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<210> 13

<211> 850

<212> DNA

<213> Pontella mediterranea

<400> 13

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aagtccacaa	agggacctct	ctccttctct	ccctacttgc	tctcccacgt	tcttggtctat	240
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aagaatggag gttactccaa cacaagaact gagaggtatg acgatggagg tatcatttct 360
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aaaaaaaaaa 850

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<210> 14
<211> 222
<212> PRT
<213> Pontella mediterranea
<400> 14

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          20          25          30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35          40          45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
          50          55          60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65          70          75          80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
          85          90          95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
          130          135          140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
          180          185          190

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Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
 210 215 220

<210> 15
 <211> 821
 <212> DNA
 <213> Unknown
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 <223> nucleic acid sequence for pdae1GFP from an unidentified
 Pontellidae species, complete cds
 <400> 15

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aacggcggat ccatgttcac ctacagaaga gttgaggagc tccacactca aactgatctt    660
ggaattgttg agtaccagca tgtattcaag actcccactg cttttgcttg aatgccatga    720
agatgaaacc tgaacaagat caatctttat ttaccacaat atgtaaattg tttaattgta    780
taattctcga gaattcatat aatacataga atttatctta c                        821

```

<210> 16
 <211> 222
 <212> PRT
 <213> Unknown
 <220>
 <223> amino acid sequence for pdae1GFP from an unidentified Pontellidae
 species
 <400> 16

Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly
 1 5 10 15
 Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly

20	25	30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser		
35	40	45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly		
50	55	60
Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn		
65	70	75
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val		
85	90	95
Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly		
100	105	110
Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe		
115	120	125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro		
130	135	140
Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu		
145	150	155
Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe		
165	170	175
Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe		
180	185	190
Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile		
195	200	205
Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala		
210	215	220

<210> 17

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the humanized version of the ppluGFP2

<400> 17

atgcccgccca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag	60
ctggtgggcg gcggagaggg ccccccgag cagggccgca tgaccaacaa gatgaagagc	120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac	240
ggcgggtaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc	360
ttccccgagg acagcgtgat cttcacgcac aagatcatcc gcagcaacgc caccgtggag	420

```

cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc      540
caccccagca tcctgcagaa cggggggcccc atgttcgcct tccgccgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca      660
ttcgccctga                                                                669

```

<210> 18

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the humanized version of the ppluGFP2

<400> 18

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
          210          215          220

```

<210> 19
 <211> 589
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage
 <400> 19

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tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt      60
ttctccatat ttgttgtctc atgttatggg ttatgggtttt tatcattttg gtacttatcc      120
atctgggttat gaaaatccat ttttgcattg tattaataat ggtgggttata ctaatactag      180
aattgaaaaa tatgaagatg gtgggtgtttt gcatgtttct ttttcttata gatatgaagc      240
tggtagagtt attggcgatt ttaaagttgt tggtactggg tttccagaag attctgttat      300
ttttactgat aaaattatta gatctaatac tactgttgaa catttgcatt caatgggtga      360
taatgttttg gttgggtctt ttgctagaac tttttctttg agagatgggtg gttattattc      420
ttttgttggt gattctcata tgcattttta atctgctatt catccatcta ttttgcaaaa      480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg      540
tattgttgaa tatcaacatg cttttaaaac tccaattgct tttgcttaa      589
```

<210> 20
 <211> 222
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the ppluGFP2 with yeast-optimized codon usage
 <400> 20

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
           20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
           35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
           50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
```

	85		90		95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly					
	100		105		110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe					
	115		120		125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro					
	130		135		140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu					
	145		150		155
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe					
	165		170		175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe					
	180		185		190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile					
	195		200		205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala					
	210		215		220

<210> 21

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopCFP mutant

<400> 21

```

atgcccgcca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag      60
ctggtggggcg gcggagaggg caccgccgag cagggccgca tgaccaacaa gatgaagagc      120
accaaaggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctggggcttt      180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac      240
ggcgggtaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc      300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc      360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag      420
cacctgcgcc ccatggggcg taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc      540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca      660
ttcgctaa

```

<210> 22

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopCFP mutant

<400> 22

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
           20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
           35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
           50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
           85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
           100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
           115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
           130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
           165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
           180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
           195          200          205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
           210          215          220

```

<210> 23

<211> 690

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA1 variant

<400> 23


```

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc      60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc      120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc      180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc      240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatcgagaa gtacgaggac      300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac      360
ttcaagggtg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc      420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc      480
ttcgcccgcg ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac      540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc      600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac      660
gccttcaaga ccccgatcgc attcgctga                                     690

```

<210> 24

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA1 variant

<400> 24

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1              5              10              15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
              20              25              30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
              35              40              45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
              50              55              60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65              70              75              80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
              85              90              95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
              100             105             110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
              115             120             125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
              130             135             140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser

```

145	150	155	160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val			
	165	170	175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu			
	180	185	190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His			
	195	200	205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr			
210	215	220	

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

atgcccgcga tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag	60
ctggtggggcg gcggagaggg cacccccagag cagggccgca tgaccaacaa gatgaagagc	120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac	240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc	360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag	420
cacctgcacc ccatgggcca taacgtgctg gtgggcagct tcgcccgcac cttcagcctg	480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcaacttcaa gagcgccatc	540
caccccagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg	600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca	660
ttcgccagat ccagagccca ggccagcaac tccgccgtgg atggcacagc cggaccggga	720
tcggccgcga ctctagatca taatcagcca taccacattt gtagaggttt tacttgcttt	780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa	819

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15

Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45

Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60

Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80

Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95

Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110

Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125

Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140

Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160

Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175

Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190

Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205

Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
          210          215          220

Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
225          230          235          240

Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
          245          250          255

Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
          260          265          270

```

<210> 27

<211> 840

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA3 variant

<400> 27

```

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc      60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcaggggccgc      120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc      180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc      240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatcgagaa gtacgaggac      300
ggcggcggtg tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac      360
ttcaagggtg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc      420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc      480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac      540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc      600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac      660
gccttcaaga ccccgatcgc attcgccaga tccagagccc aggccagcaa ctccgccgtg      720
gatggcacag ccggaccggg atcgggccgc actctagatc ataatcagcc ataccacatt      780
tgtagagggt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa      840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1              5              10              15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
              20              25              30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
              35              40              45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
              50              55              60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65              70              75              80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
              85              90              95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
              100              105              110

```

Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
 115 120 125
 Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
 130 135 140

 Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
 145 150 155 160
 Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
 165 170 175
 Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
 180 185 190
 Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
 195 200 205
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
 210 215 220
 Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
 225 230 235 240
 Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
 245 250 255
 Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
 260 265 270
 Pro Pro Pro Glu Pro Glu Thr
 275